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| NEWS | 4 | Feb 24 | TEMA now available on STN |
| NEWS | 5 | Feb 26 | NTIS now allows simultaneous left and right truncation |
| NEWS | 6 | Feb 26 | PCTFULL now contains images |
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| NEWS | 8 | Mar 24 | PATDPAFULL now available on STN |
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| NEWS | 12 | Apr 17 | Polymer searching in REGISTRY enhanced |
| NEWS | 13 | Jun 13 | Indexing from 1947 to 1956 added to records in CA/CAPLUS |
| NEWS | 14 | Apr 21 | New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX |
| NEWS | 15 | Apr 28 | RDISCLOSURE now available on STN |
| NEWS | 16 | May 05 | Pharmacokinetic information and systematic chemical names added to PHAR |
| NEWS | 17 | May 15 | MEDLINE file segment of TOXCENTER reloaded |
| NEWS | 18 | May 15 | Supporter information for ENCOMPPAT and ENCOMPLIT updated |
| NEWS | 19 | May 19 | Simultaneous left and right truncation added to WSCA |
| NEWS | 20 | May 19 | RAPRA enhanced with new search field, simultaneous left and right truncation |
| NEWS | 21 | Jun 06 | Simultaneous left and right truncation added to CBNB |
| NEWS | 22 | Jun 06 | PASCAL enhanced with additional data |
| NEWS | 23 | Jun 20 | 2003 edition of the FSTA Thesaurus is now available |
| NEWS | 24 | Jun 25 | HSDB has been reloaded |

| NEWS | EXPRESS | April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003 |
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=> file .pub

FILE 'MEDLINE' ENTERED AT 13:32:50 ON 15 JUL 2003

FILE 'BIOSIS' ENTERED AT 13:32:50 ON 15 JUL 2003
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=> s ciphergen
L1          54 CIPHERGEN


=> duplicate remove l1
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L1
L2          46 DUPLICATE REMOVE L1 (8 DUPLICATES REMOVED)


=> d 1-10 bib ab


L2    ANSWER 1 OF 46      MEDLINE
AN    2003309657      IN-PROCESS
DN    22721803   PubMed ID: 12837598
TI    Use of proteinchip array surface enhanced laser desorption/ionization
      time-of-flight mass spectrometry (seldi-tof ms) to identify thymosin
      beta-4, a differentially secreted protein from lymphoblastoid cell lines.
AU    Diamond Deborah L; Zhang Yanni; Gaiger Alexander; Smithgall Molly; Vedvick
      Thomas S; Carter Darrick
CS    Ciphergen Biosystems Inc., Fremont, California, USA.
SO    JOURNAL OF THE AMERICAN SOCIETY FOR MASS SPECTROMETRY, (2003 Jul) 14 (7)
      760-5.
      Journal code: 9010412. ISSN: 1044-0305.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    IN-PROCESS; NONINDEXED; Priority Journals
ED    Entered STN: 20030703
      Last Updated on STN: 20030703
AB    The identification of proteins differentially expressed between cancer and
      normal cells is vital for the development of cancer diagnostics,
      therapeutics and vaccines.  Using a ProteinChip Biomarker System (
      **Ciphergen** Biosystems, Fremont, CA) which combines ProteinChip
      technology with time-of-flight mass spectrometry, we have developed a
      simple method to screen and identify differentially secreted proteins from
      tumor cell lines.  Mass spectra of the range of proteins secreted from
      normal B-cells were generated along with those secreted from Epstein-Barr
      virus transformed B-cells.  A mass peak at m/z = 4972.1 that was highly
      over-represented in the transformed B-cell line was chosen for
      identification and purified by reversed phase chromatography with
      concomitant monitoring of fractions by SELDI-TOF MS.  The resulting
      purified protein was digested with trypsin and the peptide masses derived
      from the SELDI-TOF spectrum were used to search the public databases for
      protein identification.  Fragment matching of the resulting peptides
      identified the protein as thymosin beta-4.  Using LC-electrospray
      ionization MS/MS, the identity of this protein was confirmed.  Thymosin
      beta-4 is a known marker in LCLs establishing the utility of this method
      to discover and identify proteins differentially expressed between cancers
      and their matched normal counterparts.


L2    ANSWER 2 OF 46      MEDLINE

AN      2003204149      MEDLINE
DN      22609862   PubMed ID: 12724632
TI      Characterization of renal allograft rejection by urinary proteomic
        analysis.
AU      Clarke William; Silverman Benjamin C; Zhang Zhen; Chan Daniel .W; Klein
        Andrew S; Molmenti Ernesto P
CS      Department of Surgery, The Johns Hopkins University School of Medicine,
        600 North Wolfe Street, Baltimore, MD 21287-8611, USA.
SO      ANNALS OF SURGERY, (2003 May) 237 (5) 660-4; discussion 664-5.
        Journal code: 0372354. ISSN: 0003-4932.
CY      United States
DT      Journal; Article; (JOURNAL ARTICLE)
LA      English
FS      Abridged Index Medicus Journals; Priority Journals
EM      200306
ED      Entered STN: 20030502
        Last Updated on STN: 20030618
        Entered Medline: 20030617
AB      OBJECTIVE: To develop a diagnostic method with no morbidity or mortality
        for the detection of acute renal transplant rejection.  SUMMARY BACKGROUND
        DATA: Rejection constitutes the major impediment to the success of
        transplantation.  Currently available methods, including clinical
        presentation and biochemical organ function parameters, often fail to
        detect rejection until late stages of progression.  Renal biopsies have
        associated morbidity and mortality and provide only a limited sample of
        the organ.  METHODS: Thirty-four urine samples were collected from 32
        renal transplant patients at various stages posttransplantation.  Samples
        were collected from 17 transplant recipients with acute rejection and 15
        patients with no rejection.  Samples from patients less than 4 days
        posttransplant were omitted from data analysis due to the presence of
        excessive inflammatory response proteins.  Rejection status was confirmed
        by kidney biopsy.  Specimens were analyzed in triplicate using SELDI mass
        spectrometry.  The obtained spectra were subjected to bioinformatic
        analysis using ProPeak as well as CART (Classification and Regression
        Tree) algorithms to identify rejection biomarker candidates.  These
        candidates were identified by their molecular weight and ranked by their
        ability to distinguish between nonrejection and rejection based on
        receiver operating characteristic (ROC) analysis.  The candidates with the
        highest area under the ROC curve (AUC) exhibited the best diagnostic
        performance.  RESULTS: The best candidate biomarkers demonstrated highly
        successful diagnostic performance: 6.5 kd (AUC = 0.839, P <.0001), 6.7 kd
        (AUC = 0.839, P <.0001), 6.6 kd (AUC = 0.807, P <.0001), 7.1 kd (AUC =
        0.807, P <.0001), and 13.4 kd (AUC = 0.804, P <.0001).  A separate
        analysis using the CART algorithm in the **Ciphergen** Biomarker
        Pattern Software correctly classified 91% of the 34 specimens in the
        training set, giving a sensitivity of 83% and specificity of 100% using
        two separate biomarker candidates at 10.0 kd and 3.4 kd.  CONCLUSIONS:
        Biomarker candidates exist in urine that have the ability to distinguish
        between renal transplant patients with no rejection and those with acute
        rejection.  These biomarker candidates are the basis for development of a
        noninvasive method of diagnosing acute rejection without the morbidity and
        mortality associated with needle biopsy.  The combination of biomarkers
        into a panel for diagnosis leads to the possibility of enhanced diagnostic
        performance.

L2      ANSWER 3 OF 46  BIOSIS   COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN      2003:150561  BIOSIS
DN      PREV200300150561
TI      Multifactorial screening design and analysis of SELDI-TOF ProteinChip(R)
        array optimization experiments.
AU      Cordingley, H. C. (1); Roberts, S. L. L.; Tooke, P.; Armitage, J. R.;
        Lane, P. W.; Wu, W.; Wildsmith, S. E.
CS      (1) Safety Assessment, GlaxoSmithKline, The Frythe, Welwyn, Hertfordshire,
        AL6 9AR, UK: hayley_c_cordingley@gsk.com UK

SO    BioTechniques, (February 2003, 2003) Vol. 34, No. 2, pp. 364-373. print.
      ISSN: 0736-6205.
DT    Article
LA    English
AB    Surface-enhanced laser desorption/ionization time-of-flight mass
      spectrometry is a powerful tool for rapidly generating protein expression
      data (peptide and protein profiles) from a large number of samples.
      However, as with any technology, it must be optimized and reproducible for
      one to have confidence in the results. Using a classical statistical
      method called the fractional factorial design of experiments, we assessed
      the effects of 11 different experimental factors. We also developed
      several metrics that reflect trace quality and reproducibility. These were
      used to measure the effect of each individual factor, and the interactions
      between factors, to determine optimal factor settings and thus ultimately
      produce the best possible traces. Significant improvements to output
      traces were seen by simultaneously altering several parameters, either in
      the sample preparation procedure or during the matrix preparation and
      application procedure. This has led to the implementation of an improved
      method that gives a better quality, reproducible, and robust output.

L2    ANSWER 4 OF 46  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN    2003:297046  BIOSIS
DN    PREV200300297046
TI    The 13th Annual Frederick Conference on capillary electrophoresis.
AU    Weinberger, Robert (1)
CS    (1) CE Technologies, P. O. Box 140, Chappaqua, NY, 10514, USA:
      RobertWeinberger@aol.com USA
SO    American Biotechnology Laboratory, (January 2003, 2003) Vol. 21, No. 1,
      pp. 30-31. print.
      Meeting Info.: 13th Annual Frederick Conference on Capillary
      Electrophoresis (CE). Frederick, Maryland, USA October 21-22, 2002
      ISSN: 0749-3223.
DT    Conference
LA    English

L2    ANSWER 5 OF 46      MEDLINE                        DUPLICATE 1
AN    2002186404      MEDLINE
DN    21909325    PubMed ID: 11912167
TI    Identification of hepatocarcinoma-intestine-pancreas/pancreatitis-
      associated protein I as a biomarker for pancreatic ductal adenocarcinoma
      by protein biochip technology.
AU    Rosty Christophe; Christa Laurence; Kuzdzal Scott; Baldwin William M;
      Zahurak Marianna L; Carnot Francoise; Chan Daniel W; Canto Marcia;
      Lillemoe Keith D; Cameron John L; Yeo Charles J; Hruban Ralph H; Goggins
      Michael
CS    Department of Pathology, The Johns Hopkins Medical Institutions,
      Baltimore, Maryland 21205-2196, USA.
NC    P50-CA62924 (NCI)
SO    CANCER RESEARCH, (2002 Mar 15) 62 (6) 1868-75.
      Journal code: 2984705R. ISSN: 0008-5472.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    200204
ED    Entered STN: 20020403
      Last Updated on STN: 20020430
      Entered Medline: 20020429
AB    New biomarkers of pancreatic adenocarcinoma are needed to improve the
      early detection of this deadly disease.  We performed surface enhanced
      laser desorption ionization (SELDI) mass spectrometry using ProteinChip
      technology (**Ciphergen** Biosystems, Fremont, CA) to screen for
      differentially expressed proteins in pancreatic juice.  Pancreatic juice
      samples obtained from patients undergoing pancreatectomy for pancreatic

adenocarcinoma were compared with juice samples from patients with other pancreatic diseases. We identified a peak approximately 16,570 daltons present in the pancreatic juice from 10/15 (67%) of the patients with pancreatic adenocarcinoma and in the pancreatic juice from 1/7 (17%) of the patients with other pancreatic diseases. Using a ProteinChip immunoassay, we identified this differentially expressed protein as hepatocarcinoma-intestine-pancreas/pancreatitis-associated-protein I (HIP/PAP-I), a protein released from pancreatic acini during acute pancreatitis and overexpressed in hepatocellular carcinoma. We then quantified by ELISA the pancreatic juice HIP/PAP-I levels in 43 patients (28 with pancreatic adenocarcinoma, 15 with other pancreatic diseases) and the serum HIP/PAP-I levels in 98 patients (53 with pancreatic adenocarcinoma, 45 with other pancreatic diseases or healthy individuals). HIP/PAP-I levels were significantly higher in both the pancreatic juice ($P < 0.001$) and in the serum ($P < 0.001$) of patients with pancreatic adenocarcinoma compared with the control group. HIP/PAP-I levels were approximately 1000-fold higher in pancreatic juice compared with serum and the magnitude of the difference between the pancreatic adenocarcinoma group and the control group was greater in the pancreatic juice samples (143.75 +/- 235.52 microg/ml versus 6.04 +/- 7.59 microg/ml) than in the serum samples (99.96 +/- 140.66 ng/ml versus 35.25 +/- 28.44 ng/ml). In our study, patients with pancreatic juice HIP/PAP-I levels > or= 20 microg/ml were 21.9 times (95% confidence interval, 3.5-136.5; $P < 0.001$) more likely to have pancreatic adenocarcinoma than patients with levels <20 microg/ml. Immunolabeling of tissue sections revealed that the HIP/PAP-I protein was strongly expressed in acini adjacent to the invasive adenocarcinoma, but it was only rarely (1/30; 3%) expressed in the neoplastic epithelium, which suggests that the main source of HIP/PAP-I release in the pancreatic juice is acini. This low level of HIP/PAP-I expression in pancreatic adenocarcinoma was confirmed by reverse transcription-PCR: only 1 (5%) of 19 pancreatic cancer cell lines expressed HIP/PAP-I transcripts. Taken together, these data suggest that pancreatic juice measurement of HIP/PAP-I may help to identify patients with pancreatic adenocarcinoma.

AB   BACKGROUND: Surface-enhanced laser desorption/ionization (SELDI) is an
     affinity-based mass spectrometric method in which proteins of interest are
     selectively adsorbed to a chemically modified surface on a biochip,
     whereas impurities are removed by washing with buffer. This technology
     allows sensitive and high-throughput protein profiling of complex
     biological specimens. METHODS: We screened for potential tumor biomarkers
     in 169 serum samples, including samples from a cancer group of 103 breast
     cancer patients at different clinical stages [stage 0 (n = 4), stage I (n
     = 38), stage II (n = 37), and stage III (n = 24)], from a control group of
     41 healthy women, and from 25 patients with benign breast diseases.
     Diluted serum samples were applied to immobilized metal affinity capture

**Ciphergen** ProteinChip Arrays previously activated with Ni2+.
Proteins bound to the chelated metal were analyzed on a ProteinChip Reader
Model PBS II. Complex protein profiles of different diagnostic groups
were compared and analyzed using the ProPeak software package. RESULTS: A
panel of three biomarkers was selected based on their collective
contribution to the optimal separation between stage 0-I breast cancer
patients and noncancer controls. The same separation was observed using
independent test data from stage II-III breast cancer patients. Bootstrap
cross-validation demonstrated that a sensitivity of 93% for all cancer
patients and a specificity of 91% for all controls were achieved by a
composite index derived by multivariate logistic regression using the
three selected biomarkers. CONCLUSIONS: Proteomics approaches such as
SELDI mass spectrometry, in conjunction with bioinformatics tools, could
greatly facilitate the discovery of new and better biomarkers. The high
sensitivity and specificity achieved by the combined use of the selected
biomarkers show great potential for the early detection of breast cancer.

L2    ANSWER 7 OF 46  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN    2002:630094  BIOSIS
DN    PREV200200630094
TI    Identification of proteomic biomarkers in prostate cancer serum using
      ProteinChip technology.
AU    Li, Xiaohong (1); Fung, Eric; Wright, George; Zhao, Lueping
CS    (1) Division of Public Health Sciences, Fred Hutchinson Cancer Research
      Center, Seattle, WA USA
SO    Cancer Epidemiology Biomarkers & Prevention, (October, 2002) Vol. 11, No.
      10 Part 2, pp. 1198s. http://cebp.aacrjournals.org/. print.
      Meeting Info.: Proceedings of the American Association for Cancer Research
      Conference on Frontiers in Cancer Prevention Research Boston, MA, USA
      October 14-18, 2002 American Society of Preventive Oncology
      . ISSN: 1055-9965.
DT    Conference
LA    English

L2    ANSWER 8 OF 46    MEDLINE                 DUPLICATE 3
AN    2002236889     MEDLINE
DN    21932152    PubMed ID: 11934738
TI    An integrated approach utilizing artificial neural networks and SELDI mass
      spectrometry for the classification of human tumours and rapid
      identification of potential biomarkers.
AU    Ball G; Mian S; Holding F; Allibone R O; Lowe J; Ali S; Li G; McCardle S;
      Ellis I O; Creaser C; Rees R C
CS    Department of Life Sciences, Nottingham Trent University, Clifton Lane,
      Clifton, Nottingham NG11 8NS, UK.. graham.balls@ntu.ac.uk
SO    BIOINFORMATICS, (2002 Mar) 18 (3) 395-404.
      Journal code: 9808944. ISSN: 1367-4803.
CY    England: United Kingdom
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    200209
ED    Entered STN: 20020429
      Last Updated on STN: 20020921
      Entered Medline: 20020920
AB    MOTIVATION: MALDI mass spectrometry is able to elicit macromolecular
      expression data from cellular material and when used in conjunction with
      **Ciphergen** protein chip technology (also referred to as
      SELDI-Surface Enhanced Laser Desorption/Ionization), it permits a
      semi-high throughput approach to be taken with respect to sample
      processing and data acquisition. Due to the large array of data that is
      generated from a single analysis (8-10000 variables using a mass range of
      2-15 kDa-this paper) it is essential to implement the use of algorithms
      that can detect expression patterns from such large volumes of data
      correlating to a given biological/pathological phenotype from multiple

samples. If successful, the methodology could be extrapolated to larger data sets to enable the identification of validated biomarkers correlating strongly to disease progression. This would not only serve to enable tumours to be classified according to their molecular expression profile but could also focus attention upon a relatively small number of molecules that might warrant further biochemical/molecular characterization to assess their suitability as potential therapeutic targets. RESULTS: Using a multi-layer perceptron Artificial Neural Network (ANN) (Neuroshell 2) with a back propagation algorithm we have developed a prototype approach that uses a model system (comprising five low and seven high-grade human astrocytomas) to identify mass spectral peaks whose relative intensity values correlate strongly to tumour grade. Analyzing data derived from MALDI mass spectrometry in conjunction with **Ciphergen** protein chip technology we have used relative importance values, determined from the weights of trained ANNs (Balls et al., Water, Air Soil Pollut., 85, 1467-1472, 1996), to identify masses that accurately predict tumour grade. Implementing a three-stage procedure, we have screened a population of approximately 100000-120000 variables and identified two ions (m/z values of 13454 and 13457) whose relative intensity pattern was significantly reduced in high-grade astrocytoma. The data from this initial study suggests that application of ANN-based approaches can identify molecular ion patterns which strongly associate with disease grade and that its application to larger cohorts of patient material could potentially facilitate the rapid identification of validated biomarkers having significant clinical (i.e. diagnostic/prognostic) potential for the field of cancer biology. AVAILIBILITY: Neuroshell 2 is commercially available from ward systems.

L2    ANSWER 9 OF 46    BIOSIS    COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN    2002:502832    BIOSIS
DN    PREV200200502832
TI    ProteinChip technology: A new and facile method for the identification and measurement of high-density lipoproteins apoA-I and apoA-II and their glycosylated products in patients with diabetes and cardiovascular disease.
AU    Dayal, Bishambar (1); Ertel, Norman H. (1)
CS    (1) VA NJ Health Care System, East Orange, NJ, 07018: bishambar.dayal@med.va.gov, norman.ertel@med.va.gov USA
SO    Journal of Proteome Research, (July August, 2002) Vol. 1, No. 4, pp. 375-380. http://pubs.acs.org/JPR. print. ISSN: 1535-3893.
DT    Article
LA    English
AB    This paper describes a ProteinChip technology for the identification and quantification of apolipoprotein profiles in crude biological samples. Expression levels of apoA-I and apoA-II and their glycosylated products were accomplished using single 1 muL plasma samples. In the present studies, strong anionic and weak cationic exchanger ProteinChips (SAX2 and WCX2 chip surfaces) were tested, and the WCX2 chip was found to be selective for specific apolipoproteins. Using the WCX2 chip and analysis via surface-enhanced laser desorption ionization mass spectrometry (SELDI-MS), apoA-I and apoA-II were separated as sharp peaks at 28 and 17 kD and did not overlap with other serum protein peaks. Since these assays can be completed on a large number of clinical samples in approximately 1 h, further development of this technique will facilitate both epidemiological studies and therapeutic trials in assessing the role of the apolipoproteins and their glycosylated products in atherosclerosis.

L2    ANSWER 10 OF 46    MEDLINE    DUPLICATE 4
AN    2002159816    MEDLINE
DN    21888704    PubMed ID: 11891524
TI    Analysis of microdissected prostate tissue with ProteinChip arrays--a way to new insights into carcinogenesis and to diagnostic tools.
AU    Wellmann Axel; Wollscheid Volker; Lu Hong; Ma Zhan Lu; Albers Peter;

Schutze Karin; Rohde Volker; Behrens Peter; Dreschers Stefan; Ko Yon;
Wernert Nicolas
CS  Institute of Pathology, University of Bonn, D-53127 Bonn, Germany..
    axel.wellmann@uni.bonn.de

AB  Prostate carcinomas are one of the most common malignancies in western
societies. The pathogenesis of this tumor is still poorly understood.
These tumors present with two characteristic features:
epithelial-mesenchymal interactions, which play a pivotal role for tumor
development and most of clinically manifest cancers arise in prostate
proper compared to a minority of tumors which develop in the transitional
zone. Deciphering the epithelial-mesenchymal cross talk and
identification of molecular pecularities of the sub-populations of cells
in different zones can therefore help understanding carcinogenesis and
development of new, non-invasive tools for the diagnosis and prognosis of
prostate carcinomas which has remained a challenge until today. A
ProteinChip array technology (SELDI = surface enhanced laser desorption
ionization) has been developed recently by **Ciphergen** Biosystems
enabling analysis and profiling of complex protein mixtures from a few
cells. This study describes the analysis of approximately 500-1000
freshly obtained prostate cells by SELDI-TOF-MS (surface enhanced laser
desorption ionization time-of-flight mass spectrometry). Pure cell
populations of stroma, epithelium and tumor cells were selected by laser
assisted microdissection. Multiple specific protein patterns were
reproducibly detected in the range from 1.5 to 30 kDa in 28
sub-populations of 4 tumorous prostates and 1 control. A specific 4.3 kDa
peak was increased in the prostate tumor stroma compared to normal
prostate proper and transitional zone stroma and increased in prostate
tumor glands compared to normal prostate proper and transitional zone
glands. Coupling laser assisted microdissection with SELDI provides
tremendous opportunities to identify cell and tumor specific proteins to
understand molecular events underlying prostate carcinoma development. It
underlines the vast potential of this technology to better understand
pathogenesis and identify potential candidates for new specific biomarkers
in general which could help to screen for and distinguish disease
entities, i.e. between clinically significant and insignificant carcinomas
of the prostate.

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    FILE 'MEDLINE, BIOSIS' ENTERED AT 13:32:50 ON 15 JUL 2003
L1          54 S CIPHERGEN
L2          46 DUPLICATE REMOVE L1 (8 DUPLICATES REMOVED)

=> s l2 and py<2001
L3          7 L2 AND PY<2001

=> d 1-7 bib ab

L3    ANSWER 1 OF 7      MEDLINE
AN    2001227489      MEDLINE
DN    21156490    PubMed ID: 11257925
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AB    This article presents current trends and advances in protein biochip
      technologies that rely upon extraction and retention of target proteins
      from liquid media.  Analytical strengths as well as technical challenges
      for these evolving platforms are presented with particular emphasis on
      selectivity, sensitivity, throughput and utility in the post-genome era.
      A general review of protein biochip technology is provided, which
      delineates approaches for protein biochip format and operation, as well as
      protein detection.  A focused discussion of three protein biochip
      technologies, Biomolecular Interaction Analysis (Biacore, Uppsala,
      Sweden), Surface Enhanced Laser Desorption/Ionisation (SELDI) ProteinChip
      Arrays (**Ciphergen** Biosystems, Fremont, CA, USA) and Fluorescent
      Planar Wave Guide (Zeptosens, Witterswil, Switzerland), follows along with
      examples of relevant applications.

ED    Entered STN: 20010322
      Last Updated on STN: 20010322
      Entered Medline: 20010125

AB    beta-Amyloid (Abeta), a 39-43 residue peptide, is the principal component
      of senile plaques found in the brains of patients with Alzheimer's disease
      (AD). There are two main lines of evidence that its deposition is the
      cause of neurodegeneration. First, mutations found in three genes in
      familial Alzheimer's cases give rise to increased production of the
      longest, most toxic, form, Abeta 1-42. Second. aggregated Abeta is toxic
      to neuronal cells in culture. Inhibitors of the proteases involved in its
      release from the amyloid precursor protein are, therefore, of major
      therapeutic interest. The best candidates for the releasing proteases are
      both aspartyl proteases, which are integrated into the membranes of the
      endoplasmic reticulum and Golgi network. A sensitive assay using
      **Ciphergen**'s Seldi system has been developed to measure all the
      variants of Abeta in culture supernatants, which will be of great value in
      screening inhibitors of these proteases. With this assay, it has been ·
      shown that increasing intracellular cholesterol increases the activities
      of both beta-secretase, and gamma-secretase 42. Moreover, changing the
      intracellular targeting of amyloid precursor glycoprotein (APP) yields
      increased alpha-secretase cleavage, and increases in the amounts of
      oxidized/nitrated forms of Abeta.

L3    ANSWER 4 OF 7      MEDLINE
AN    2000097082      MEDLINE
DN    20097082    PubMed ID: 10631507
TI    Profiling of amyloid beta peptide variants using SELDI Protein Chip
      arrays.
AU    Davies H; Lomas L; Austen B
CS    Ciphergen Biosystems, Surry, UK.
SO    BIOTECHNIQUES, **(1999 Dec)** 27 (6) 1258-61.
      Journal code: 8306785. ISSN: 0736-6205.
CY    United States
DT    Journal; Article; (JOURNAL ARTICLE)
LA    English
FS    Priority Journals
EM    200002
ED    Entered STN: 20000218
      Last Updated on STN: 20000218
      Entered Medline: 20000209

AB    The profile of amyloid beta (A beta) peptide variants secreted into the
      media of human cultured cells that express the amyloid precursor protein
      was examined by Surface Enhanced Laser Desorption/Ionization (SELDI)
      ProteinChip technology from **Ciphergen** Biosystems using
      biologically active ProteinChip Arrays. An anti-A beta polyclonal
      antibody (anti-NTA4) was used to capture and purify multiple
      immunoreactive A beta fragments from a single microliter of media onto the
      ProteinChip Array. Fragments retained on the surface of the ProteinChip
      Array were detected directly by mass in the ProteinChip System to provide
      detailed information on the identity of different A beta variants secreted
      from the cultured cells. We discuss existing and potential applications
      of this immunoassay for the detection and relative quantitation of A beta
      species from both cultured cell systems and clinical samples.

L3    ANSWER 5 OF 7  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN    2001:312003  BIOSIS
DN    PREV200100312003
TI    The application of protein chip surface-enhanced laser
      desorption/ionization (SELDI) mass spectrometry for the identification of
      proteins in chronic lymphocytic leukemia.
AU    Czader, M. (1); Kuzdzal, S. (1); Flinn, I. (1); Byrd, J.; Chan, D. (1);
      Borowitz, M. J. (1)
CS    (1) Johns Hopkins Medical Institutions, Baltimore, MD USA
SO    Blood, **(November 16, 2000)** Vol. 96, No. 11 Part 1, pp. 579a.

print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology
San Francisco, California, USA December 01-05, 2000 American Society of
Hematology
. ISSN: 0006-4971.

DT  Conference
LA  English
SL  English
AB  There is a scarcity of data on protein modifications related to the
    malignant behavior of hematologic malignancies including chronic
    lymphocytic leukemia (CLL). This is partly due to the technical
    difficulties in the purification and identification of small amounts of
    protein, which in contrast to nucleic acid, can not be readily amplified.
    SELDI mass spectrometry makes it possible to rapidly determine the
    molecular weights of sample proteins using as few as 2 X 105 cells. It
    provides femtomole-level sensitivity for proteins ranging from 1 to more
    than 300 kD. In addition, the identification of the protein can be
    accomplished on the same protein chip array on which the initial analysis
    was started. This technique has been used to identify unique protein
    markers in malignancies including prostate cancer. We applied SELDI to a
    series of cases of CLL and other lymphoproliferative disorders previously
    characterized by four color flow cytometry. These included 9 cases of
    classical CLL, 2 cases of atypical CLL expressing bright CD20 and/or CD79b
    but positive for CD5 and CD23, and 1 case of a CD5 negative B-cell
    lymphoproliferative disorder. Abnormal lymphocytes accounted for at least
    90% of cells in all cases. Lysed whole blood specimens were extracted with
    triton X100 and applied to highly selective protein chips, washed under
    selective conditions, and analyzed by SELDI (**Ciphergen**
    Biosystems, Palo Alto, CA). Aliquots of either normal peripheral blood or
    flow-sorted CD19+ normal B cells were similarly treated. There were
    numerous protein peaks throughout the range 1-300kD that were common to
    all leukemic samples, normal peripheral blood and flow-sorted B-cells. In
    addition, however, there were three unique peaks of 11.3kD and 13.8kD and
    14.0kD found only in the leukemic samples. The same unique proteins were
    seen with both non-polar and hydrophobic chips, and were common to all 9
    CLL samples. They were also present in both cases of atypical CLL, and the
    CD5-negative lymphoproliferative disorder, indicating the similarity of
    these disorders and CLL. We conclude that SELDI technology may be used to
    screen for proteins that can distinguish B-cell lymphoproliferative
    disorders from normal blood and normal B cells. Investigation of new chip
    surfaces and use of additional wash conditions may reveal additional
    disease-associated markers. Further characterization of these unique
    proteins is underway to understand the role they may play in the
    pathogenesis of these disorders.

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AN  2001:49474  BIOSIS
DN  PREV200100049474
TI  Beyond the Human Genome.
AU  Ezzell, Carol
SO  Scientific American, (**July, 2000**) Vol. 283, No. 1, pp. 64-69.
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    ISSN: 0036-8733.
DT  Article
LA  English
SL  English

L3  ANSWER 7 OF 7  BIOSIS  COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AN  2000:483757  BIOSIS
DN  PREV200000483757
TI  A rapid protein profiling system that speeds study of cancer and other
    diseases.
AU  Rubin, Richard B. (1); Merchant, Maggie (1)
CS  (1) Ciphergen Biosystems, Inc., 6611 Dumbarton Cir., Fremont, CA, 94555

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
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| FULL ESTIMATED COST | 22.65 | 22.86 |

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